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**Description**Field of the Invention

- 5 This invention relates to an improved method for expressing DNA encoding the bone morphogenetic protein-2 family in mammalian cells.

Description of Related Art

- 10 The disorders associated with bone loss present major public health problems for Western societies. Osteoporosis alone may affect 20 million Americans in the early years of the next century. Hence, there is wide interest in identifying factors or potential therapeutic agents that inhibit bone loss and stimulate the formation of healthy new bone.

- Bone is an extremely complex, but highly organized, connective tissue that is continuously remodeled during the life of an adult by cellular events that initially break it down (osteoclastic resorption) and then rebuild it (osteoblastic formation). This remodeling process occurs in discrete packets throughout the skeleton, i.e., in both cortical bone and trabecular bone. It has recently been reported that mouse bone marrow cells can be stimulated to generate osteoclasts in the presence of parathyroid hormone-related protein or vitamin D. See Akatsu et al., Endocrinology, 125: 20-27 (1989); Takahashi et al., Endocrinology, 123: 2600-2602 (1988) and Takahashi et al., Endocrinology, 123: 1504-1510 (1988).

- The currently available therapeutic agents known to stimulate bone formation are fluoride, estrogen, metabolites, and vitamin D. Fluoride clearly increases trabecular bone mass, but questions remain about the quality of the new bone formed, the side effects observed in some patients, whether there are beneficial effects on vertebral fracture rates, and whether increased fragility of cortical bone with subsequent propensity to hip fracture follows.

- Another approach is using agents that promote resorption (parathyroid hormone) and then interrupt resorption (calcitonin). One proposed, but not validated, such sequential therapeutic regimen is coherence therapy, where bone metabolic units are activated by oral phosphate administration and then resorption is inhibited by either diphosphonates or calcitonin.

- 30 Within the past few years several factors that stimulate osteoblasts have been identified in bone, including transforming growth factor- $\beta$  (TGF- $\beta$ ), fibroblast growth factor, platelet-derived growth factor, insulin-like growth factor-I, and  $\beta$ 2 macroglobulin.

- Other proteins stored in the bone matrix may also be important for bone formation. When demineralized bone was injected into the muscle or subcutaneous tissue of rats, a cascade of events, including chondrogenesis, ensued. Urist, Science, 150: 893 (1965). Since the 1960s several investigators have attempted to identify and characterize this activity and have provided an assay for purification of such activity. Reddi and Huggins, Proc. Natl. Acad. Sci. USA, 69: 1601-1605 (1972); Sampath and Reddi, Proc. Natl. Acad. Sci. USA, 78: 7599-7603 (1981).

- This assay served as the basis for purifying several novel proteins from bone in sufficient quantity and purity to provide amino acid sequence information, including osteogenin, a protein of 22 Kd [Sampath et al., Proc. Natl. Acad. Sci. USA, 84: 7109 (1987); Luyten et al., J. Biol. Chem., 264: 13377-13380 (1989)] and a glycoprotein called osteoinductive factor [Bentz et al., J. Cell. Biol., 107: 162a (1989)]. See also Wang et al., Proc. Natl. Acad. Sci., 85: 9484-9488 (1988). Based on amino acid sequence data, clones encoding several proteins related by sequence similarity to TGF- $\beta$  were isolated from bovine and human sources. Wozney et al., Science, 242: 1528-1534 (1988); PCT WO 88/00205 published January 14, 1988; U.S. 4,877,864 issued October 31, 1989. These latter proteins included BMP-2A (also known as BMP-2), BMP-2B (also known as BMP-4), and BMP-3. The sequence of tryptic peptides from osteogenin match the sequence reported for BMP-3.

- The TGF- $\beta$  supergene family includes five distinct forms of TGF- $\beta$  [Sporn and Roberts, in Peptide Growth Factors and Their Receptors, Sporn and Roberts, eds. (Springer-Verlag: Berlin, 1990) pp. 419-472], as well as the differentiation factors vg1 [Weeks and Melton, Cell, 51: 861-867 (1987)] and DPP-C polypeptide [Padgett et al., Nature, 325: 81-84 (1987)], the hormones activin and inhibin [Mason et al., Nature, 318: 659-663 (1985); Mason et al., Growth Factors, 1: 77-88 (1987)], the Mullerian-inhibiting substance, MIS [Cate et al., Cell, 45: 685-698 (1986)], the BMPs, and the developmentally regulated protein Vgr-1 [Lyons et al., Proc. Natl. Acad. Sci. USA, 86: 4554-4558 (1989)]. The subset BMP-2A and BMP-2B is approximately 75% homologous in sequence to DPP-C and may represent the mammalian equivalent of that protein.

The proteins of the TGF- $\beta$  supergene family are disulfide-linked homo- or heterodimers encoded by larger precursor polypeptide chains containing a hydrophobic signal sequence, a long and relatively poorly conserved N-terminal pro region of several hundred amino acids, a cleavage site (usually polybasic), and a shorter and more highly conserved C-terminal region. This C-terminal region corresponds to the processed mature protein and contains approximately 100 amino acids with a characteristic cysteine motif, i.e., the conservation of seven of the nine cysteine residues of TGF- $\beta$  among all known family members. Although the position of the cleavage site between the mature and pro regions varies among the family members, the C-terminus of all of the proteins is in the identical position, ending in the sequence Cys-X-Cys-X, but differing in every case from the TGF- $\beta$  consensus C-terminus of Cys-Lys-Cys-Ser. Sporn and Roberts, 1990, *supra*.

The pro region of TGF- $\beta$  associates non-covalently with the mature TGF- $\beta$  dimer (Wakefield et al., *J. Biol. Chem.*, 263: 7646-7654 (1988); Wakefield et al., *Growth Factors*, 1: 203-218 (1989)], and the pro regions are found to be necessary for proper folding and secretion of the active mature dimers of both TGF- $\beta$  and activin [Gray and Mason, *Science*, 247: 1328-1330 (1990)]. The association between the mature and pro regions of TGF- $\beta$  masks the biological activity of the mature dimer, resulting in formation of an inactive latent form. Latency is not a constant of the TGF- $\beta$  supergene family, since the presence of the pro region has no effect on activin or inhibin biological activity.

A unifying feature of the biology of the proteins from the TGF- $\beta$  supergene family is their ability to regulate developmental processes. Regarding bone formation *in vivo*, of all the proteins in the TGF- $\beta$  supergene family, the BMPs and TGF- $\beta$  play the most major role.

Recombinant TGF- $\beta$ 1 has been cloned [Derynck et al., *Nature*, 316:701-705 (1985)] and expressed in Chinese hamster ovary cells [Gentry et al., *Mol. Cell. Biol.*, 7: 3418-3427 (1987)]. Additionally, recombinant human TGF- $\beta$ 2 [deMartin et al., *EMBO J.*, 6: 3673 (1987)], as well as human and porcine TGF- $\beta$ 3 [Derynck et al., *EMBO J.*, 7: 3737-3743 (1988); ten Dijke et al., *Proc. Natl. Acad. Sci. USA*, 85: 4715 (1988)], have been cloned. Expression levels of the mature TGF- $\beta$ 1 protein in COS cells are increased by substituting a serine residue for cysteine residues located in the pro region of the TGF- $\beta$ 1 precursor. Brunner et al., *J. Biol. Chem.*, 264: 13660-13664 (1989)].

BMP-2A and BMP-3 have been recombinantly produced in monkey COS-1 cells and Chinese hamster ovary cells by Wozney et al., *supra*. However, the level of expression of BMP-2A and -2B cDNA is relatively low when the DNA is not amplified. Higher levels of BMP-2A protein expression in CHO cells have been obtained by amplification to a high copy number using methotrexate selection of dihydrofolate reductase. Wang et al., *Proc. Natl. Acad. Sci. USA*, 87: 2220-2224 (1990).

Confirmation of the osteogenic activity of BMPs and commercial production thereof depend on the ability to produce useful amounts of active material by recombinant means of expression and development of methods to purify them in an active form. The ability to successfully reconstitute endochondral bone formation remains the standard by which to judge the osteogenic character of candidate factors. The biological activities of BMP-2A, BMP-3, and an unrelated molecule, BMP-1, were originally assessed in an implant model using material expressed in COS cells, resulting in only cartilage formation. Wozney et al., *supra*. More recently, the partially purified BMP-2A expressed in CHO cells was shown to require a dose of at least 600 ng/implant to induce cartilage and bone formation. Wang et al., 1990, *supra*. The osteogenic activities of BMP-2B and BMP-3 have not been established.

It is an object of the present invention to provide purified BMP-2B in sufficient quantities to test for its osteogenic activity, and to produce it on a commercial scale.

It is another object to improve the expression levels of BMP-2 DNA in mammalian cells without amplifying the DNA.

It is still another object to achieve higher production of BMP-2 protein than was previously attained at a level of amplification equivalent to that previously employed.

These and other objects will be apparent to those of ordinary skill in the art of molecular biology.

## 50 Summary of the Invention

Accordingly, this invention provides a DNA construct comprising DNA encoding a mature BMP-2 upstream of which is DNA encoding a precursor portion of a mammalian protein other than that of BMP-2. Preferably, the precursor portion has at least 25% amino acid sequence identity to the native precursor portion of the BMP-2 in the region spanning the N-terminus of the BMP-2 precursor to the first cysteine residue in the mature BMP-2.

In another aspect, this invention provides an expression vector comprising the above-described DNA construct and hosts transformed with such a vector.

In a method for expressing DNA encoding a BMP-2 in mammalian cells, this invention also furnishes the improvement which comprises employing as the host the host transformed with the vector described above.

Additionally, this invention provides a method for producing BMP-2 by culturing mammalian host cells transfected with the expression vector described above, the cells being capable of expressing the DNA construct of the vector, and recovering mature BMP-2 from the cells. Preferably, the recovery is from the host cell media (in which case the expression vector contains a signal sequence, whether native to the precursor or BMP-2 or heterologous to the precursor or BMP-2, that directs secretion of the mature BMP-2 to the medium).

The result of this method is dramatically improved expression levels of BMP-2 DNA in mammalian cells over that attainable using the BMP-2 precursor portion that is native to the BMP-2 to be produced.

#### Brief Description of the Drawings

Figure 1 depicts the amino acid sequences of BMP-2A and BMP-2B and indicates the regions of sequence identity. The junction between the precursor portions and mature portions is shown by a vertical line with two arms.

Figure 2 depicts the complete amino acid sequence of the chimera of the precursor portion of BMP-2A and the mature region of BMP-2B.

Figure 3A depicts expression plasmid pRK5.bmp2/4-1.1, and Figure 3B depicts the junction region of the BMP-2A/2B hybrid insert. A portion of an alignment of BMP-2A and BMP-2B is shown with identical residues boxed. The coding sequence resulting from fusion of BMP-2A and BMP-2B is shaded showing the crossover point. The underlined sequence with an arrow indicates sequence confirmed by Edman degradation of purified recombinant BMP-2B.

Figure 4 depicts a fluorogram of an SDS-PAGE reducing gel of supernatants from human embryonic kidney cell line transfections with DNA encoding either the native BMP-2A molecule (lane 1), the chimeric BMP-2A/2B molecule (lane 2), the native BMP-2B molecule (lane 3), control pRK5 plasmid (lane 4), or no plasmid (lane 5). Figure 5 depicts graphs of calcium content (Fig. 5A) and alkaline phosphatase content (Fig. 5B) of implants in rats (harvested at 12 days) of demineralized bone powder (DBP) or guanidine-HCl-extracted DBP reconstituted with the indicated amounts of mature recombinant BMP-2B or TGF- $\beta$ . The solid and cross-hatched bars presented for two doses are duplicate runs.

#### Description of the Preferred Embodiments

##### Definitions

As used herein, the term "BMP-2" refers to the family of bone morphogenetic proteins of the type 2, derived from any species. Reference to BMP-2 herein is understood to be a reference to any one of the currently identified forms, including BMP-2A and BMP-2B (formerly called BMP-4) described by Wozney et al., *supra*, and WO 88/00205, *supra*, the sequences of which are shown in Figure 1, as well as to BMP-2 species identified in the future. The term "BMP-2" also includes polypeptides derived from the sequence of any known BMP-2 whose mature sequence is at least about 75% homologous with the sequence of a mature BMP-2, including DPP-C. Members of the BMP-2 family appear to be encoded as a larger precursor that shares a region of high homology near the N-terminus.

As used herein, "precursor portion" refers to the polypeptide sequence derived from a prepro-mammalian protein representing either the pro-domain or prepro-domain without the mature protein. Candidate mammalian proteins having such precursor portions are those encoded as larger precursors that typically contain a signal sequence at their N-terminus followed by a dibasic amino acid cleavage site and a pro-region, followed by another dibasic amino acid cleavage site and the mature region of the protein. Thus, the precursor portion is that which is N-terminal to the mature N-terminus of the mammalian protein and may include the signal sequence for secretion of that protein. Preferably, the mammalian protein from which the precursor portion is derived is a member of the TGF- $\beta$  supergene family, as described above. Examples of suitable precursor portions are those wherein the signal sequence is followed by a sequence that represents a polypeptide region that after cleavage reassociates with the mature protein covalently or non-covalently, as in the case of insulin, relaxin, inhibin, activin, and TGF- $\beta$ .

The expression "at least 25% amino acid sequence identity to the native precursor portion of the BMP-2 from the N-terminus of the BMP-2 precursor to the first cysteine residue in the mature region of the BMP-2" refers to a precursor portion that shares this minimum sequence identity to the relevant portion of the

BMP-2 DNA being expressed. This sequence identity can be readily calculated for BMP-2A and BMP-2B from the entire amino acid sequences shown in Figure 1. As examples, the precursor portion of BMP-2A shares 55% amino acid sequence identity to the native precursor portion of BMP-2B from the N-terminus of the BMP-2B precursor to the first cysteine residue in the mature region of the BMP-2B molecule, and vice-versa. The precursor of the protein vgr [Lyons et al., *Proc. Natl. Acad. Sci. USA*, 86: 4554-4558 (1989)], which is related to the product of an amphibian gene vg1 expressed in frog oocytes, shares 25% homology with the relevant portion of BMP-2B. The protein decapenta-plegic gene complex from *Drosophila*, DPP-C [Padgett et al., *Nature*, 325: 81-84 (1987)], shares 27% and 28% amino acid sequence identity with the relevant portions of BMP-2A and BMP-2B, respectively. Most preferred herein is the use of the BMP-2A prepro-domain as the precursor portion for secreting mature BMP-2B.

#### Modes for Carrying Out the Invention

The vectors and methods disclosed herein are suitable for use for expression in a wide range of mammalian host cell lines.

In general, prokaryotes such as, e.g., *E. coli* strains are preferred for cloning, amplifying, or storing the vectors of interest. Vector DNA is easily obtainable from certain prokaryotes. *E. coli* K12 strain MM 294 (ATCC No. 31,446) is particularly useful for this purpose, as are *E. coli* B and *E. coli* X1776 (ATCC No. 31,537). In general, plasmid vectors containing replicon and control sequences that are derived from species compatible with the host cell are used in connection with these prokaryotic hosts. The vector ordinarily carries a replication site, as well as marking sequences that are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically transformed using pBR322, a plasmid derived from an *E. coli* species [see, e.g., Bolivar et al., *Gene*, 2: 95 (1977)]. pBR322 contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR322 plasmid, or other microbial plasmid or phage, must also contain, or be modified to contain, promoters that can be used by the microbial organism for expression of the selectable marker genes.

Cultures of cells derived from mammalian organisms are useful as expression hosts using tissue culture methods [Tissue Culture, Academic Press, Kruse and Patterson, editors (1973)]. Examples of such useful host cell lines include monkey kidney CV1 line transformed by SV40 sequences (COS-7, ATCC CRL 1651); human embryonic kidney line [293, Graham et al., *J. Gen. Virol.*, 36: 59 (1977)]; baby hamster kidney cells (BHK, ATCC CCL 10); Chinese hamster ovary cells [CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77: 4216 (1980)]; mouse sertoli cells [TM4, Mather, *Biol. Reprod.*, 23: 243-251 (1980)]; monkey kidney cells (CV1, ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); human cervical carcinoma cells (HELA, ATCC CCL 2); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); mouse mammary tumor cells (MMT 060562, ATCC CCL51); rat hepatoma cells [HTC, M1.54, Baumann et al., *J. Cell. Biol.*, 85: 1-8 (1980)]; and TRI cells [Mather et al., *Annals N.Y. Acad. Sci.*, 383: 44-68 (1982)]. The most preferred mammalian hosts herein are CHO and 293 cell lines.

Expression vectors for such cells ordinarily will contain control regions, which are specific sequences at the 5' and 3' ends of eukaryotic genes that may be involved in the control of either transcription, RNA processing, or translation. At the 3' end of most eukaryotic genes is an AATAAA sequence that signals processing of the mRNA for polyadenylation addition.

Thus, the vector will typically include a promoter located in front of the gene to be expressed, polyadenylation sites, and transcriptional terminator sequences, all described in further detail herein. The vector may optionally also include an origin of replication. Further, the vector may contain, after the promoter, a transcription initiation site located in front of an optional splice unit, which is in turn located before the encoding gene.

Examples of suitable mammalian expression vectors are found in EP 307,247; 260,148; 309,237; and 307,248.

For use in mammalian cells, the control functions on the expression vectors are often provided by viral material. For example, commonly used promoters are derived from the genomes of polyoma, Adenovirus2, retroviruses, cytomegalovirus, and Simian Virus 40 (SV40). Other promoters are those from heterologous sources, e.g., the beta actin promoter. The early and late promoters of SV40 virus are particularly useful because both are obtained easily from the virus as a fragment that also contains the SV40 viral origin of replication [Fiers et al., *Nature*, 273: 113 (1978)]. Smaller or larger SV40 fragments may also be used, provided there is included the approximately 250-bp sequence extending from the HindIII site toward the BglI site located in the viral origin of replication. The immediate early promoter of the human cytomegalovirus is conveniently obtained as a HindIII restriction fragment. Greenaway et al., *Gene*, 18: 355-

360 (1982). Further, it is also possible, and often desirable, to utilize promoter or control sequences normally associated with the desired gene sequence, provided such control sequences are compatible with the host cell systems.

Transcription of a DNA encoding a desired heterologous polypeptide by higher eukaryotes is increased by inserting an enhancer sequence into the vector. The enhancer is a cis-acting element of DNA, usually about from 10 to 300 bp, that acts on a promoter to enhance its transcription-initiation activity. Enhancers are relatively orientation and position independent, having been found 5', [Laimins et al., *Proc. Natl. Acad. Sci. USA*, 78: 993 (1981)] and 3' [Lusky et al., *Mol. Cell Bio.*, 3: 1108 (1983)] to the transcription unit, within an intron [Banerji et al., *Cell*, 33: 729 (1983)] as well as within the coding sequence itself [Osborne et al., *Mol. Cell Bio.*, 4: 1293 (1984)]. Preferably, however, the enhancer element is located upstream of the promoter sequence for this invention. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin,  $\alpha$ -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. One preferred enhancer is the SV40 enhancer region.

Expression vectors used in mammalian host cells will also contain polyadenylation sites. Examples of polyadenylation regions are those derived from viruses such as e.g., the SV40 (early and late) or HBV.

An origin of replication may be provided either by construction of the vector to include an exogenous origin, such as may be derived from SV40 or other viral (eg., Polyoma, Adeno, VSV, BPV) source, or may be provided by the host cell. If the vector is integrated into the host cell chromosome, the latter is often sufficient.

The expression vectors may suitably contain a selection gene, also termed a selectable marker. A selection gene encodes a protein necessary for the survival or growth of a host cell transformed with the vector. Examples of suitable selectable markers for mammalian cells include dihydrofolate reductase (DHFR), thymidine kinase (TK), or neomycin. When such selectable markers are successfully transferred into a mammalian host cell, the transformed mammalian host cell can survive if placed under selective pressure.

There are two widely used distinct categories of selective regimes. The first category is based on the metabolism of a cell and the use of a mutant cell line that lacks the ability to grow independent of a supplemented medium. Two examples are CHO DHFR<sup>-</sup> cells and mouse LTK<sup>-</sup> cells. These cells lack the ability to grow without the addition of such nutrients as thymidine or hypoxanthine. Because these cells lack certain genes necessary for a complete nucleotide synthesis pathway, they cannot survive unless the missing nucleotides are provided in a supplemented medium. An alternative to supplementing the medium is to introduce an intact DHFR or TK gene into cells lacking the respective genes, thus altering their growth requirements. Individual cells that were not transformed with the DHFR or TK gene will not be capable of survival in non-supplemented medium. Therefore, direct selection of those cells requires cell growth in the absence of supplemental nutrients.

The second category is dominant selection, which refers to a selection scheme that does not require the use of a mutant cell line. This method typically employs a drug to arrest growth of a host cell. Those cells that have a novel gene would express a protein conveying drug resistance and would survive the selection. Examples of drugs used in dominant selection include neomycin [Southern and Berg, *J. Molec. Appl. Genet.*, 1: 327 (1982)], mycophenolic acid [Mulligan and Berg, *Science*, 209: 1422 (1980)], or hygromycin [Sugden et al., *Mol. Cell. Biol.*, 5: 410-413 (1985)]. The three examples given above employ bacterial genes under eukaryotic control to convey resistance to the appropriate drug, i.e., neomycin (G418 or geneticin), xgpt (mycophenolic acid), or hygromycin, respectively.

Extremely good amounts of polypeptide are produced by transiently transfected cell cultures using the method of this invention. It is also expected that stable transformants would result in higher production levels of the BMP-2 than transformants with the native proBMP-2 sequence. Furthermore, the process herein is expected to enhance production levels further when the cells are cotransfected with a separate vector encoding a secondary coding sequence. One secondary coding sequence comprises dihydrofolate reductase (DHFR) that is affected by an externally controlled parameter, such as methotrexate (MTX), thus permitting control of expression by control of the MTX concentration.

#### Typical Methodology Employable

Construction of suitable vectors containing the desired coding and control sequences employs standard recombinant techniques. Isolated plasmids or DNA fragments are cleaved, tailored, and re-ligated to form the desired plasmid.

If flush ends are required, the cleaved DNA preparation may be treated for 30 minutes at 37°C with DNA Polymerase I (Klenow fragment) or T4 DNA polymerase, phenol-chloroform extracted, and ethanol precipitated. 3' protruding ends are removed by the 3' to 5' exonucleolytic activity of either enzyme, and the 5' protruding ends are made flush by the 5' to 3' polymerase activity incorporating complementary nucleotide until the end of the fragment is reached.

Size separation of the cleaved fragments may be performed using 6 percent polyacrylamide gel described by Goeddel et al., Nucleic Acids Res., 8: 4057 (1980).

For analysis to confirm correct sequences in plasmids constructed, the ligation mixtures are typically used to transform *E. coli* K12 strain 294 (ATCC 31,446) or other suitable *E. coli* strains, and successful transformants selected by ampicillin or tetracycline resistance where appropriate. Plasmids from the transformants are prepared and analyzed by restriction mapping and/or DNA sequencing by the method of Messing et al., Nucleic Acids Res., 9: 309 (1981) or by the method of Maxam et al., Meth. Enzym., 65: 499 (1980).

If amplification of the sequences is desired, DHFR-protein-coding DNA sequences are introduced into the mammalian cell host and stable transfectants are selected in the medium. The host cell cultures are grown in the presence of approximately 200-500 nM concentrations of methotrexate, a competitive inhibitor of DHFR activity. The effective range of concentration is highly dependent, of course, upon the nature of the DHFR gene and the characteristics of the host. Clearly, generally defined upper and lower limits cannot be ascertained. Suitable concentrations of other folic acid analogs or other compounds that inhibit DHFR could also be used. MTX itself is, however, convenient, readily available, and effective.

In order to simplify the examples and claims, certain frequently occurring methods will be referenced by shorthand phrases.

"Transfection" refers to the taking up of an expression vector by a host cell whether or not any coding sequences are in fact expressed. Numerous methods of transfection are known to the ordinarily skilled artisan, for example, CaPO<sub>4</sub> and electroporation. Successful transfection is generally recognized when any indication of the operation of this vector occurs within the host cell.

"Transformation" means introducing DNA into an organism so that the DNA is replicable, either as an extrachromosomal element or by chromosomal integrant. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described by Cohen, S.N. Proc. Natl. Acad. Sci. (USA), 69: 2110 (1972); Mandel et al., J. Mol. Biol. 53:154 (1970); and more recently Liljestrom et al., Gene, 40: 241-246 (1985), is generally used for prokaryotes or other cells that contain substantial cell-wall barriers. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52: 456-457 (1978) is preferred. General aspects of mammalian cell host system transformations have been described by Axel in U.S. Pat. No. 4,399,216 issued August 16, 1983. Transformations into yeast are typically carried out according to the method of Van Solingen, et al., J. Bact., 130: 946 (1977) and Hsiao, et al., Proc. Natl. Acad. Sci. (USA) 76: 3829 (1979). However, other methods for introducing DNA into cells such as by nuclear injection or by protoplast fusion may also be used.

"Operably linked" refers to juxtaposition such that the normal function of the components can be performed. Thus, a coding sequence "operably linked" to control sequences refers to a configuration wherein the coding sequence can be expressed under the control of these sequences and wherein the DNA sequences being linked are contiguous and, in the case of a secretory leader, contiguous and in reading phase. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it effects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, then synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

"Control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, a ribosome binding site, and possibly, other as yet poorly understood sequences. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

"Expression system" refers to DNA sequences containing a desired coding sequence and control sequences in operable linkage, so that hosts transformed with these sequences are capable of producing the encoded proteins. To effect transformation, the expression system may be included on a vector; however, the relevant DNA may then also be integrated into the host chromosome.

As used herein, "cell," "cell line," and "cell culture" are used interchangeably and all such designations include progeny. Thus, "transformants" or "transformed cells" includes the initial transformant and cultures derived therefrom without regard for the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. Mutant progeny that have the same functionality as screened for in the originally transformed cell are included. Where distinct designations are intended, it will be clear from the context.

"Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are commercially available, are publicly available on an unrestricted basis, or can be constructed from such available plasmids in accord with published procedures. In addition, other equivalent plasmids are known in the art and will be apparent to the ordinary artisan.

"Digestion" of DNA refers to catalytic cleavage of the DNA with an enzyme that acts only at specific nucleotide sequences in the DNA. Such enzymes are called restriction enzymes, and the sequence for which each is specific is called a restriction site. The various restriction enzymes used herein are commercially available and their reaction conditions, cofactors, and other requirements as established by the enzyme suppliers are used. Restriction enzymes commonly are designated by abbreviations composed of a capital letter followed by other letters representing the microorganism from which each restriction enzyme originally was obtained and then a number designating the particular enzyme. In general, about 1 µg of plasmid or DNA fragment is used with about 1-2 units of enzyme in about 20 µl of buffer solution. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation of about 1 hour at 37 °C is ordinarily used, but may vary in accordance with the supplier's instructions. After incubation, protein is removed by extraction with phenol and chloroform, and the digested nucleic acid is recovered from the aqueous fraction by precipitation with ethanol. When appropriate, digestion with a restriction enzyme is followed by bacterial alkaline phosphatase-mediated hydrolysis of the terminal 5' phosphates to prevent the two ends of a DNA fragment from "circularizing," or forming a closed loop that would impede insertion of another DNA fragment at the restriction site. Unless otherwise stated, digestion of plasmids is not followed by 5' terminal dephosphorylation. Procedures and reagents for dephosphorylation are conventional [Maniatis et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory, 1982) pp. 133-134].

"Recovery or "isolation" of a given fragment of DNA from a restriction digest means separation of the digest on polyacrylamide or agarose gel by electrophoresis, identification of the fragment of interest by comparison of its mobility versus that of marker DNA fragments of known molecular weight, removal of the gel section containing the desired fragment, and separation of the gel from DNA. This procedure is known generally. For example, see R. Lawn et al., Nucleic Acids Res. 9: 6103-6114 (1981), and D. Goeddel et al., Nucleic Acids Res. 8: 4057 (1980).

"Ligation" refers to the process of forming phosphodiester bonds between two double-stranded nucleic acid fragments [T. Maniatis et al., 1982, *supra*, p. 146]. Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units of T4 DNA ligase ("ligase") per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

"Preparation" of DNA from transformants means isolating plasmid DNA from microbial culture. Unless otherwise provided, the alkaline/SDS method of Maniatis et al., 1982, *supra*, p. 90, may be used.

"Oligonucleotides" are short-length, single- or double- stranded polydeoxynucleotides that are chemically synthesized by known methods [such as phosphotriester, phosphite, or phosphoramidite chemistry, using solid-phase techniques such as described in EP Pat. Pub. No. 266,032 published May 4, 1988, or via deoxynucleoside H-phosphonate intermediates as described by Froehler et al., Nucl. Acids Res., 14: 5399-5407 (1986)]. They are then purified on polyacrylamide gels.

The following example is intended to illustrate specific embodiments now known for practicing the invention, but the invention is not to be considered limited thereto.

#### EXAMPLE 1

cDNAs for BMP-2A and BMP-2B were cloned from a human placental cDNA library constructed in lambda gt10 [Ullrich et al., Nature, 313: 756-761 (1985)] using oligonucleotide probes based on the human nucleotide sequence [Wozney et al., *supra*] using standard cloning techniques [Sambrook et al., Molecular Cloning: A Laboratory Manual, Second Ed. (Cold Spring Harbor Laboratory, New York, 1989)]. The probes employed were as follows (where the initiator ATG is underlined and the direction from left to right is 5' to 3'):



BMP-2A Probes

CGACCATGGTGGCCGGGACCCGCTGTCTTCTAGCGTTGCTGCTTCCCCAGGTCCTCCTGG

5 GCGGCGCG (for 5' end)

AATGAAAAGGTTGTATTAAAGAACTATCAGGACATGGTTGTGGAGGGTTGTGGGTGTCGC

(for 3' end)

10

BMP-2B Probes

ATGATTCTGGTAACCGAATGCTGATGGTCGTTTTATTATGCCAAGTCCTGCTAGGAGGC

15 GCGAGCCATGCTAGTTTG (for 5' end)

CAGGAGATGGTAGTAGAGGGATGTGGGTGCCGCTGAGATCAGGCAGTCCTTGAGGATAG

ACAG (for 3' end)

20

No clones for BMP-3 were found in the human placental cDNA library using a similar approach to that above. Several cell lines were screened for expression of BMP-3 RNA by polymerase chain reaction amplification of the RNA [Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51: 263-273 (1986)] using oligonucleotide primers based on the human nucleotide sequence [Wozney et al., *supra*]. One positive cell line, the NCI-H69 human small-cell lung carcinoma [Gazdar et al., *Cancer Res.*, 40: 3502-3507 (1980)] was identified. A cDNA library was prepared from the mRNA and screened with oligonucleotide probes using standard techniques (Sambrook et al., *supra*). The probe sequences were as follows (where the direction from left to right is 5' to 3'):

30 AGTGTCCCGCAGCGACGCCGGGAGCCGACGCGCCGCGCGGGTACCTAGCC (for 5' end)

TACCCTAACATGACAGTAGAGTCTTGCGCTTGAGATAACCTGGCAAAGA (for 3' end)

Positive lambda gt10 clones were identified for BMP-2A, BMP-2B, and BMP-3 proteins, and these clones were sequenced. The sequenced clones encoding the BMP-2A and BMP-2B full-length proteins were digested with *Sall*. The expression vector pRK5 [EP 307,247 published 3/15/89] was also digested with *Sall* and the gel-isolated large fragment was ligated with the cDNA *Sall* digests encoding each BMP to create the expression plasmids pRK5.bmp2a and pRK5.bmp2b, for BMP-2A and BMP-2B, respectively.

The sequenced clone encoding the BMP-3 full-length protein was digested with *EcoRI*. pRK5 was also digested with *EcoRI* and the gel-isolated large fragment was ligated with the cDNA *EcoRI* digest encoding BMP-3 to create the expression plasmid pRK5.bmp3.

40 A human embryonic kidney cell line (293) [Graham et al., *supra*] was grown to confluence on 60-mm plates in F12:DMEM (1:1) medium (Gibco) containing 10% fetal calf serum (FCS) and transfected with one of the three BMP expression plasmids by the calcium phosphate method [Gorman, *DNA Cloning*, Vol. II (ed. Glover, D.), 143-190 (IRL, Oxford, 1985)]. More specifically, 5-10  $\mu$ g of one of the three BMP plasmid DNAs was mixed with 1  $\mu$ g of DNA encoding the VA RNA gene (Thimmappaya et al., *Cell*, 31: 543 (1982)) and dissolved in 250  $\mu$ l of 0.25 M  $\text{CaCl}_2$ . Added to this (dropwise while vortexing) was 250  $\mu$ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM  $\text{NaPO}_4$ , and the precipitate was allowed to form for 5-10 min. at 25°C. The suspended precipitate was then added to the cells and allowed to settle for 4-5 hours in the incubator. The medium was then aspirated off, the cell layer was washed with 5 ml of F12:DMEM (1:1), and 0.5 ml of 20% glycerol in phosphate-buffered saline (PBS) was added for 30 sec. A total of 5 ml of F12:DMEM (1:1) containing 10% fetal bovine serum was added, aspirated off, and replenished. 24 to 48 hours later, the 10% fetal bovine serum medium was replaced with serum-free F12:DMEM (1:1) minus cysteine and methionine. The cells were incubated for 2 hours at 37°C in 5%  $\text{CO}_2$  in the presence of 200  $\mu\text{Ci/ml}$   $^{35}\text{S}$ -cysteine and 200  $\mu\text{Ci/ml}$   $^{35}\text{S}$ -methionine. Then the cell layers were washed with PBS and F12:DMEM (1:1) containing cysteine and methionine was added and the cells were allowed to incubate for 5-7 hours. Conditioned medium was then collected, concentrated 5-fold by lyophilization, and loaded on a 15% SDS gel, which was soaked with Enhance® (New England Nuclear) gel scintillation fluid, dried, and exposed to film at -80°C for 12 hours. Metabolic labeling of the conditioned medium revealed detectable levels of expression that were low as compared with transfections of similar vectors containing activin or TGF- $\beta$  cDNAs.

Conditioned medium from the cells transfected with BMP-2A, BMP-2B, or BMP-3 was partially purified by heparin-Sepharose chromatography as follows. A 5-ml heparin-Sepharose CL6B (Pharmacia) column was initially equilibrated with 4 M urea, 20 mM TrisCl at pH 7. Then the conditioned medium in 4 M urea, 20 mM TrisCl, pH 7, was loaded on the column. After loading, the fractions were eluted stepwise with 0, 0.1, 0.5 and 2.0 M NaCl in 4 M urea, 20 mM TrisCl, pH 7. The bone-forming activity of the fractions of each step was assessed *in vivo* by the method of Sampath and Reddi, *supra*. Both BMP-2A and BMP-2B possessed easily demonstrable activity, but BMP-3 activity was more difficult to demonstrate. Not all transfections gave biologically active material. These data suggest that expression levels of BMP-3 are substantially lower than those of BMP-2A and BMP-2B using native precursors.

Next, the role of the precursor region on formation and secretion of mature BMP-2B was examined. An expression plasmid containing DNA encoding the N-terminal prodomain of BMP-2A spliced to the C-terminal mature growth factor domain of BMP-2B (the sequence of which is shown in Figure 2) was assembled. This hybrid BMP-2A/2B construct codes for a protein of 400 amino acids, consisting of residues 1-268 from BMP-2A and residues 277-409 of BMP-2B. The hybrid was assembled from the BMP-2A plasmid (pRK5.bmp2a) by removing the region from the Ball site to the HindIII site and replacing it with the corresponding Ball to HindIII fragment from the BMP-2B plasmid (pRK5.bmp2b).

The resulting expression plasmid (designated pRK5.bmp2/4-1.1) is shown in Figure 3A. Nucleotide sequencing revealed two differences in the BMP-2A sequence compared to that reported in W088/00205 *supra*: a substitution of A for G at base 261 relative to the ATG start codon, which is silent, and an A for T substitution at base 570 that results in an Arg instead of a Ser at residue 190. (The sequence in Figure 1 does not reflect the newly found difference at position 190.) The 2A/2B insert sequence is shown in Figure 3B. *E. coli* MM294 cells transformed with this plasmid (*E. coli* MM294/pRK5.bmp2/4-1.1) were deposited with the American Type Culture Collection on May 23, 1990 under ATCC Accession No. 68,330.

pRK5.bmp2/4-1.1, as well as pRK5.bmp2a and pRK5.bmp2b for comparative purposes, were used to transfect 293 cells using the same procedure as described above, and the transfected cells were metabolically labeled using the same procedure as described above, except that they were labeled for four hours with 250  $\mu$ Ci/ml each of the  $^{35}$ S-labeled methionine and cysteine. They were then applied to a 10% SDS-PAGE gel (reduced) using the procedure described above. Figure 4 is the fluorogram exposed for 12 hours at  $-80^{\circ}\text{C}$  of this gel (reduced) of conditioned media (5  $\mu$ l/lane) from the 293 cells transfected with plasmids containing either BMP-2A (lane 1), BMP-2A/2B (lane 2), BMP-2B (lane 3), control pRK5 plasmid (lane 4), or no plasmid (lane 5).

For the hybrid, strong bands were found at 36 kD and 23 kD corresponding to the pro and mature forms, respectively. The full-length BMP-2A construct expressed mostly the 36-kD band of the pro form with a small amount of the 18-kD mature form, while for the full-length BMP-2B construct, only a small amount of the 23-kD mature band was found. Thus, greatly enhanced expression of the DNA encoding the BMP-2B mature dimer was observed over expression with the native prod domains.

Biologically active recombinant BMP-2B homodimers were purified from 3-10 liters of conditioned medium from 293 cultures (in 150-mm dishes) transiently transfected with pRK5.bmp2/4-1.1 and DNA encoding the VA RNA gene [Thimmappaya et al., *supra*] as described above but using 28  $\mu$ g pRK5.bmp2/4-1.1 and 8  $\mu$ g VA gene per dish. One hour after glycerol shock, the media was replaced with serum-free medium [F12:DMEM (1:1) supplemented with 5  $\mu$ g/ml human transferrin, 10  $\mu$ g/ml insulin, and optionally 10 ng/ml epidermal growth factor, Mather, *Biol. Reprod.*, 23: 243 (1980)] (20 ml of media in each plate). The cells were incubated for 24 hours, the media was harvested, and then fresh medium was added; the cells were incubated again for 24 hours, the medium was harvested and fresh medium was added; and this cycle was repeated once again for a total of three harvests at 24, 48, and 72 hours.

Under the conditions of harvesting, the BMP-2B accumulates in the medium to about 200 ng/ml, while background protein levels remain relatively low, as estimated by the intensity of silver-stained SDS-PAGE gels of the conditioned medium. The protein was purified as follows: A 30-ml heparin-Sepharose CL6B column (Pharmacia) was initially equilibrated with 4 M urea, 20 mM TrisCl at pH 7. Then the conditioned medium in 4 M urea, 20 mM TrisCl, pH 7, was loaded on the column. The fractions were eluted with a 500-ml gradient of 0 to 0.5 M NaCl in 4 M urea, 20 mM TrisCl, pH 7. One major protein band appeared on the SDS-PAGE gel of the pooled fractions, with an estimated 70-80% purity.

The pooled fractions were concentrated with an Amicon Centricon® 10 concentrator about 10-fold, then diluted about 10-fold with 4 M urea, 20 mM Tris, pH 7. The diluted material was loaded onto a 1-ml Pharmacia Mono-Q HR 5/5 column and was eluted with a 0 to 0.3 M NaCl gradient (30 ml) in 4 M urea, 20 mM Tris, pH 7. The peak fractions were pooled, and determined to be about 95% pure by SDS-PAGE. The pooled fractions were dialyzed against 0.1 M acetic acid, lyophilized, and redissolved in 1 ml of 0.1 M acetic acid.

In cases where the purity of the Mono-Q column eluate was judged unsatisfactory, an additional HPLC purification step was employed. This step involved loading the pooled fractions from the Mono-Q column directly on a Vydac C4 RP-HPLC column (100 x 2.1 mm). The HPLC column was eluted with a 30-ml gradient of 0 to 40% N-propanol, 0.1 to 0.06% trifluoroacetic acid. The pooled material from this third step was approximately 95% pure, as judged by SDS gel electrophoresis. This material was lyophilized and redissolved as described above. Final yield of purified mature BMP-2B was determined by quantitative amino acid analysis; the preparation with the three steps yielded 10 µg/liter of conditioned medium, or approximately 5% overall based on SDS gel analysis.

N-terminal amino acid sequencing of the purified mature BMP-2B showed a single amino terminal sequence beginning at residue 285 of BMP-2A/2B (residue 294 of BMP-2B). Sequence data was collected for 18 cycles, and matched exactly that shown underlined in Fig. 3B. No minor sequence was observed. The prominent 36-Kd band observed in the SDS gel of the transfected supernatants was identified as the pro region by amino terminal sequencing after transfer to PVDV membranes. Cleavage of the signal sequence between residues 23 and 24 (...LLGGAAG:LVPELGRRKFAAA) was as predicted by the weight matrix method of von Heijne, *Nucl. Acid Res.*, **144**: 683-690 (1986). No cleavage at the nearby RRK sequence was observed.

Recombinant BMP-2B is a disulfide-linked dimer, as shown by a decrease in apparent molecular weight on SDS gel electrophoresis from 33 Kd in the absence of reductants to 23 Kd in the presence of reductants. BMP-2B has two consensus sites for N-glycosylation.

The HPLC-purified recombinant BMP-2B was tested in the bone formation assay of Reddi and Sampath, *supra*, along with TGF- $\beta$  and a control. In this assay the implants placed into rats were 25 mg demineralized bone powder (DBP) or 25 mg guanidine-HCl-extracted DBP reconstituted with 0, 0.5, 2.0, or 6.0 µg of the purified recombinant BMP-2B or 1 µg recombinant mature human TGF- $\beta$ 1 (U.S. Pat. No. 4,886,747 issued December 12, 1989). The implants were harvested at 12 days, and the calcium content (Fig. 5A) was measured by atomic absorption spectrophotometry and the alkaline phosphatase content (Fig. 5B) was measured by hydrolysis of p-nitrophenyl phosphate. Duplicate experiments of the 0.5 and 2.0 doses of BMP-2B indicated by solid and cross-hatched bars in Fig. 5 were performed.

A significant increase in calcium content (even over DBP, which contains some BMP) was seen with the 2 µg dose of BMP-2B, while the 0.5 µg dose was sufficient to increase alkaline phosphatase. After a 12-day harvest, implants of guanidine-HCl-extracted DBP alone or reconstituted with 1 µg of purified recombinant BMP-2B were fixed and mounted without decalcification. Three-micron sections were cut and stained with haematoxylin and eosin. Microscopic examination of these stained sections showed abundant bone formation in implants reconstituted with BMP-2B as indicated by the presence of calcium deposits. Implants reconstituted with vehicle alone did not form bone.

A construct of the BMP-2A prodomain with the BMP-3 mature region prepared as described above (by replacing the small Ball to HindIII fragment of pRK5.bmp2a with the corresponding Ball-HindIII fragment from pRK5.bmp3) was transfected into 293 cells as described above. In this case, the expression level was no better than the expression levels of the native prosequences for BMP-2A and BMP-3. This experiment shows that the BMP-2A prodomain does not improve expression levels of every member of the entire BMP family, but rather is effective in enhancing expression of DNA encoding the BMP-2 family.

The ability of the heterologous precursor region to improve secretion of the biologically active dimer may reflect a preference of the BMP-2A precursor region for the BMP-2B mature growth factor sequence. It certainly indicates the importance of the precursor region in proper expression and folding of the biologically active mature dimer form in the BMP-2 family.

#### Deposit of Materials

The following culture has been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

Strain	ATCC Dep. No.	Deposit Date
MM294/pRK5.bmp2/4-1.1	68,330	May 23, 1990

This deposit was made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture for 30 years from the date of deposit. The organism will be made available by ATCC under the terms of the Budapest Treaty, and subject to an

agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

In respect of those designations in which a European patent is sought, a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which the application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample. (Rule 28(4) EPC)

The assignee of the present application has agreed that if the culture on deposit should die or be lost or destroyed when cultivated under suitable conditions, it will be promptly replaced on notification with a viable specimen of the same culture. Availability of the deposited strain is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of one aspect of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustration that it represents. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: GENENTECH, INC.
- (ii) TITLE OF INVENTION: Mammalian Expression of the BMP-2 Family
- (iii) NUMBER OF SEQUENCES: 12
- 10 (iv) CORRESPONDENCE ADDRESS:  
 (A) ADDRESSEE: Genentech, Inc.  
 (B) STREET: 460 Point San Bruno Blvd  
 (C) CITY: South San Francisco  
 (D) STATE: California  
 (E) COUNTRY: USA  
 (F) ZIP: 94080
- 15 (v) COMPUTER READABLE FORM:  
 (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 (B) COMPUTER: IBM PC compatible  
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 (D) SOFTWARE: patin (Genentech)
- 20 (vi) CURRENT APPLICATION DATA:  
 (A) APPLICATION NUMBER:  
 (B) FILING DATE:  
 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
 (A) APPLICATION NUMBER: U.S. Ser. No. 07/528,300  
 25 (B) FILING DATE: 24 May 1990
- (viii) ATTORNEY/AGENT INFORMATION:  
 (A) NAME: Hasak, Janet E.  
 (B) REGISTRATION NUMBER: 28,616  
 (C) REFERENCE/DOCKET NUMBER: 623
- 30 (ix) TELECOMMUNICATION INFORMATION:  
 (A) TELEPHONE: 415/266-1896  
 (B) TELEFAX: 415/952-9881  
 (C) TELEX: 910/371-7168

(2) INFORMATION FOR SEQ ID NO:1:

- 35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 68 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGACCATGGT GGCCGGGACC CGCTGTCTTC TAGCGTTGCT GCTTCCCCAG 50

GTCCTCCTGG GCGGCGCG 68

(2) INFORMATION FOR SEQ ID NO:2:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 bases  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATGAAAAGG TTGTATTAAA GAACTATCAG GACATGGTTG TGGAGGGTTG 50

TGGGTGTCGC 60

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGATTCTTG GTAACCGAAT GCTGATGGTC GTTTTATTAT GCCAAGTCCT 50

GCTAGGAGGC GCGAGCCATG CTAGTTTG 78

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGGAGATGG TAGTAGAGGG ATGTGGGTGC CGCTGAGATC AGGCAGTCCT 50

TGAGGATAGA CAG 63

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGTGTCCCGC AGCGACGCCG GGAGCCGACG CGCCGCGCGG GTACCTAGCC 50

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACCCTAACA TGACAGTAGA GTCTTGCGCT TGCAGATAAC CTGGCAAAGA 50

5

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

15

Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg  
 1 5 10 15  
 Lys Phe Ala Ala Ala  
 20

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

25

Met Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln  
 1 5 10 15  
 Val Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg  
 20 25 30  
 Arg Lys Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro  
 35 40 45  
 Ser Asp Glu Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met  
 50 55 60  
 Phe Gly Leu Lys Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val  
 65 70 75  
 Pro Pro Tyr Met Leu Asp Leu Tyr Arg Arg His Ser Gly Gln Pro  
 80 85 90  
 Gly Ser Pro Ala Pro Asp His Arg Leu Glu Arg Ala Ala Ser Arg  
 95 100 105  
 Ala Asn Thr Val Arg Ser Phe His His Glu Glu Ser Leu Glu Glu  
 110 115 120  
 Leu Pro Glu Thr Ser Gly Lys Thr Thr Arg Arg Phe Phe Phe Asn  
 125 130 135  
 Leu Ser Ser Ile Pro Thr Glu Glu Phe Ile Thr Ser Ala Glu Leu  
 140 145 150  
 Gln Val Phe Arg Glu Gln Met Gln Asp Ala Leu Gly Asn Asn Ser  
 155 160 165  
 Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile Ile Lys Pro Ala  
 170 175 180  
 Thr Ala Asn Ser Lys Phe Pro Val Thr Ser Leu Leu Asp Thr Arg

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		185		190		195
	Leu Val Asn Gln	Asn Ala Ser Arg Trp	Glu Ser Phe Asp Val Thr			
		200	205			210
5	Pro Ala Val Met	Arg Trp Thr Ala Gln	Gly His Ala Asn His Gly			
		215	220			225
	Phe Val Val Glu	Val Ala His Leu Glu	Glu Lys Gln Gly Val Ser			
		230	235			240
10	Lys Arg His Val	Arg Ile Ser Arg Ser	Leu His Gln Asp Glu His			
		245	250			255
	Ser Trp Ser Gln	Ile Arg Pro Leu Leu	Val Thr Phe Gly His Asp			
		260	265			270
15	Gly Lys Gly His	Pro Leu His Lys Arg	Glu Lys Arg Gln Ala Lys			
		275	280			285
	His Lys Gln Arg	Lys Arg Leu Lys Ser	Ser Cys Lys Arg His Pro			
		290	295			300
	Leu Tyr Val Asp	Phe Ser Asp Val Gly	Trp Asn Asp Trp Ile Val			
20		305	310			315
	Ala Pro Pro Gly	Tyr His Ala Phe Tyr	Cys His Gly Glu Cys Pro			
		320	325			330
	Phe Pro Leu Ala	Asp His Leu Asn Ser	Thr Asn His Ala Ile Val			
		335	340			345
25	Gln Thr Leu Val	Asn Ser Val Asn Ser	Lys Ile Pro Lys Ala Cys			
		350	355			360
	Cys Val Pro Thr	Glu Leu Ser Ala Ile	Ser Met Leu Tyr Leu Asp			
		365	370			375
30	Glu Asn Glu Lys	Val Val Leu Lys Asn	Tyr Gln Asp Met Val Val			
		380	385			390
	Glu Gly Cys Gly	Cys Arg				
		395 396				

## (2) INFORMATION FOR SEQ ID NO:9:

35

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 409 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

45

50

55

Met Ile Pro Gly Asn Arg Met Leu Met	Val Val Leu Leu Cys Gln
1 5 10	15
Val Leu Leu Gly Gly Ala Ser His Ala Ser	Leu Ile Pro Glu Thr
20 25	30
Gly Lys Lys Lys Val Ala Glu Ile Gln Gly	His Ala Gly Gly Arg
35 40	45
Arg Ser Gly Gln Ser His Glu Leu Leu Arg	Asp Phe Glu Ala Thr
50 55	60
Leu Leu Gln Met Phe Gly Leu Arg Arg Arg	Pro Gln Pro Ser Lys
65 70	75



	Ser	Ala	Val	Ile	Pro	Asp	Tyr	Met	Arg	Asp	Leu	Tyr	Arg	Leu	Gln	80	85	90
5	Ser	Gly	Glu	Glu	Glu	Glu	Gln	Ile	His	Ser	Thr	Gly	Leu	Glu		95	100	105
	Tyr	Pro	Glu	Arg	Pro	Ala	Ser	Arg	Ala	Asn	Thr	Val	Arg	Ser	Phe	110	115	120
10	His	His	Glu	Glu	His	Leu	Glu	Asn	Ile	Pro	Gly	Thr	Ser	Glu	Asn	125	130	135
	Ser	Ala	Phe	Arg	Phe	Leu	Phe	Asn	Leu	Ser	Ser	Ile	Pro	Glu	Asn	140	145	150
	Glu	Val	Ile	Ser	Ser	Ala	Glu	Leu	Arg	Leu	Phe	Arg	Glu	Gln	Val	155	160	165
15	Asp	Gln	Gly	Pro	Asp	Trp	Glu	Arg	Gly	Phe	His	Arg	Ile	Asn	Ile	170	175	180
	Tyr	Glu	Val	Met	Lys	Pro	Pro	Ala	Glu	Val	Val	Pro	Gly	His	Leu	185	190	195
20	Ile	Thr	Arg	Leu	Leu	Asp	Thr	Arg	Leu	Val	His	His	Asn	Val	Thr	200	205	210
	Arg	Trp	Glu	Thr	Phe	Asp	Val	Ser	Pro	Ala	Val	Leu	Arg	Trp	Thr	215	220	225
25	Arg	Glu	Lys	Gln	Pro	Asn	Tyr	Gly	Leu	Ala	Ile	Glu	Val	Thr	His	230	235	240
	Leu	His	Gln	Thr	Arg	Thr	His	Gln	Gly	Gln	His	Val	Arg	Ile	Ser	245	250	255
	Arg	Ser	Leu	Pro	Gln	Gly	Ser	Gly	Asn	Trp	Ala	Gln	Leu	Arg	Pro	260	265	270
30	Leu	Leu	Val	Thr	Phe	Gly	His	Asp	Gly	Arg	Gly	His	Ala	Leu	Thr	275	280	285
	Arg	Arg	Arg	Arg	Ala	Lys	Arg	Ser	Pro	Lys	His	His	Ser	Gln	Arg	290	295	300
35	Ala	Arg	Lys	Lys	Asn	Lys	Asn	Cys	Arg	Arg	His	Ser	Leu	Tyr	Val	305	310	315
	Asp	Phe	Ser	Asp	Val	Gly	Trp	Asn	Asp	Trp	Ile	Val	Ala	Pro	Pro	320	325	330
40	Gly	Tyr	Gln	Ala	Phe	Tyr	Cys	His	Gly	Asp	Cys	Pro	Phe	Pro	Leu	335	340	345
	Ala	Asp	His	Leu	Asn	Ser	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	350	355	360
45	Val	Asn	Ser	Val	Asn	Ser	Ser	Ile	Pro	Lys	Ala	Cys	Cys	Val	Pro	365	370	375
	Thr	Glu	Leu	Ser	Ala	Ile	Ser	Met	Leu	Tyr	Leu	Asp	Glu	Tyr	Asp	380	385	390
	Lys	Val	Val	Leu	Lys	Asn	Tyr	Gln	Glu	Met	Val	Val	Glu	Gly	Cys	395	400	405
50	Gly	Cys	Arg															
55																		

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5	Met	Val	Ala	Gly	Thr	Arg	Cys	Leu	Leu	Ala	Leu	Leu	Leu	Pro	Gln	1	5	10	15
10	Val	Leu	Leu	Gly	Gly	Ala	Ala	Gly	Leu	Val	Pro	Glu	Leu	Gly	Arg	20	25	30	
	Arg	Lys	Phe	Ala	Ala	Ala	Ser	Ser	Gly	Arg	Pro	Ser	Ser	Gln	Pro	35	40	45	
15	Ser	Asp	Glu	Val	Leu	Ser	Glu	Phe	Glu	Leu	Arg	Leu	Leu	Ser	Met	50	55	60	
	Phe	Gly	Leu	Lys	Gln	Arg	Pro	Thr	Pro	Ser	Arg	Asp	Ala	Val	Val	65	70	75	
20	Pro	Pro	Tyr	Met	Leu	Asp	Leu	Tyr	Arg	Arg	His	Ser	Gly	Gln	Pro	80	85	90	
	Gly	Ser	Pro	Ala	Pro	Asp	His	Arg	Leu	Glu	Arg	Ala	Ala	Ser	Arg	95	100	105	
25	Ala	Asn	Thr	Val	Arg	Ser	Phe	His	His	Glu	Glu	Ser	Leu	Glu	Glu	110	115	120	
	Leu	Pro	Glu	Thr	Ser	Gly	Lys	Thr	Thr	Arg	Arg	Phe	Phe	Phe	Asn	125	130	135	
30	Leu	Ser	Ser	Ile	Pro	Thr	Glu	Glu	Phe	Ile	Thr	Ser	Ala	Glu	Leu	140	145	150	
	Gln	Val	Phe	Arg	Glu	Gln	Met	Gln	Asp	Ala	Leu	Gly	Asn	Asn	Ser	155	160	165	
35	Ser	Phe	His	His	Arg	Ile	Asn	Ile	Tyr	Glu	Ile	Ile	Lys	Pro	Ala	170	175	180	
	Thr	Ala	Asn	Ser	Lys	Phe	Pro	Val	Thr	Arg	Leu	Leu	Asp	Thr	Arg	185	190	195	
40	Leu	Val	Asn	Gln	Asn	Ala	Ser	Arg	Trp	Glu	Ser	Phe	Asp	Val	Thr	200	205	210	
	Pro	Ala	Val	Met	Arg	Trp	Thr	Ala	Gln	Gly	His	Ala	Asn	His	Gly	215	220	225	
45	Phe	Val	Val	Glu	Val	Ala	His	Leu	Glu	Glu	Lys	Gln	Gly	Val	Ser	230	235	240	
	Lys	Arg	His	Val	Arg	Ile	Ser	Arg	Ser	Leu	His	Gln	Asp	Glu	His	245	250	255	
50	Ser	Trp	Ser	Gln	Ile	Arg	Pro	Leu	Leu	Val	Thr	Phe	Gly	His	Asp	260	265	270	
	Gly	Arg	Gly	His	Ala	Leu	Thr	Arg	Arg	Arg	Arg	Ala	Lys	Arg	Ser	275	280	285	
55	Pro	Lys	His	His	Ser	Gln	Arg	Ala	Arg	Lys	Lys	Asn	Lys	Asn	Cys	290	295	300	

Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn  
 305 310 315  
 Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His  
 320 325 330  
 Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn  
 335 340 345  
 His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile  
 350 355 360  
 Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met  
 365 370 375  
 Leu Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln  
 380 385 390  
 Glu Met Val Val Glu Gly Cys Gly Cys Arg  
 395 400

## (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 56 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His  
 1 5 10 15  
 Ser Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp  
 20 25 30  
 Gly Lys Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys  
 35 40 45  
 His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys  
 50 55 56

## (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Gln His Val Arg Ile Ser Arg Ser Leu Pro Gln Gly Ser Gly  
 1 5 10 15  
 Asn Asn Ala Gln Leu Arg Pro Leu Leu Val Thr Phe Gly His Asp  
 20 25 30  
 Gly Arg Gly His Ala Leu Thr Arg Arg Arg Arg Ala Lys Arg Ser  
 35 40 45  
 Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys  
 50 55 60

## Claims

55 Claims for the following Contracting States : AT, BE, CH, DE, DK, FR, GB, GR, IT, LI, LU, NL, SE

1. A DNA hybrid construct comprising in the 5' to 3' direction a DNA sequence for the precursor portion of BMP-2A operably linked to a DNA sequence encoding mature BMP-2B.

2. The DNA construct of claim 1 wherein the precursor portion comprises a signal sequence.
3. The DNA construct of claim 1 or claim 2 wherein both the BMP-2A and BMP-2B are human BMPs.
- 5 4. An expression vector comprising the DNA construct of any one of claims 1 to 3.
5. An expression vector that is pRK5.bmp2/4-1.1, available from deposit ATCC 68,330.
6. A mammalian host cell transformed with the expression vector of claim 4.
- 10 7. A mammalian host cell transformed with the expression vector of claim 5.
8. An E.coli host cell transformed with the expression vector of claim 5.
- 15 9. A method for expressing DNA encoding mature BMP-2B in mammalian cells, comprising employing the host cell of claim 6.
10. A method for expressing DNA encoding mature BMP-2B in mammalian cells, comprising employing the host cell of claim 7.

20 **Claims for the following Contracting State : ES**

1. A method which comprises construction of DNA hybrid construct comprising in the 5' to 3' direction a DNA sequence for the precursor portion of BMP-2A operably linked to a DNA sequence encoding mature BMP-2B.
- 25 2. The method of claim 1 wherein the precursor portion comprises a signal sequence.
3. The method of claim 1 or claim 2 wherein both the BMP-2A and BMP-2B are human BMPs.
- 30 4. A method which comprises construction of an expression vector comprising a DNA hybrid construct comprising in the 5' to 3' direction a DNA sequence for the precursor portion of BMP-2A operably linked to a DNA sequence encoding mature BMP-2B.
- 35 5. A method according to claim 4 wherein the precursor portion comprises a signal sequence.
6. A method according to claim 4 or claim 5 wherein both the BMP-2A and BMP-2B are human BMPs.
7. A method comprising transformation of a mammalian host cell with an expression vector comprising a DNA hybrid construct comprising in the 5' to 3' direction a DNA sequence for the precursor portion of BMP-2A operably linked to a DNA sequence encoding mature BMP-2B.
- 40 8. A method according to claim 7 wherein the precursor portion comprises a signal sequence.
9. A method according to claim 7 or claim 8 wherein both the BMP-2A and BMP-2B are human BMPs.
10. A method comprising transforming a mammalian host cell with expression vector pRK5.bmp 2/4-1.1, available from deposit ATCC 68,330.
- 50 11. A method comprising transforming a E.coli host cell with expression vector pRK5.bmp 2/4-1.1, available from deposit ATCC 68,330.
12. A method for expressing DNA encoding mature BMP-2B in mammalian cells, comprising employing a mammalian host cell transformed with a DNA hybrid construct comprising in the 5' to 3' direction a DNA sequence for the precursor portion of BMP-2A operably linked to a DNA sequence encoding mature BMP-2B.
- 55 13. A method according to claim 12 wherein the precursor portion comprises a signal sequence.

14. A method according to claim 12 or claim 13 wherein both the BMP-2A and BMP-2B are human BMPs.

15. A method for expressing DNA encoding mature BMP-2B in mammalian cells, comprising employing a mammalian host cell transformed with expression vector pRK5.bmp 2/4-1.1, available from deposit  
5 ATCC 68,330.

#### Patentansprüche

Patentansprüche für folgende Vertragsstaaten : AT, BE, CH, DE, DK, FR, GB, GR, IT, LI, LU, NL, SE

- 10 1. DNA-Hybrid-Konstrukt, das in der 5' zu 3'-Richtung eine DNA-Sequenz für den Vorläuferabschnitt von BMP-2A, die operabel mit einer für reifen BMP-2B kodierenden DNA-Sequenz verbunden ist, aufweist.
2. DNA-Konstrukt nach Anspruch 1, worin der Vorläuferabschnitt eine Signalsequenz aufweist.
- 15 3. DNA-Konstrukt nach Anspruch 1 oder 2, worin sowohl BMP-2A als auch BMP-2B menschliche BMPs sind.
4. Expressionsvektor, umfassend das DNA-Konstrukt nach einem der Ansprüche 1 bis 3.
- 20 5. Expressionsvektor, der pRK5.bmp2/4-1.1 ist, erhältlich vom Depot ATCC 68.330.
6. Säugetierwirtszelle, transformiert mit dem Expressionvektor nach Anspruch 4.
7. Säugetierwirtszelle, transformiert mit dem Expressionvektor nach Anspruch 5.
- 25 8. E.coli-Wirtszelle, transformiert mit dem Expressionvektor nach Anspruch 5.
9. Verfahren zum Exprimieren von für reifen BMP-2B kodierender DNA in Säugetierzellen, das die Verwendung der Wirtszelle nach Anspruch 6 umfaßt.
- 30 10. Verfahren zum Exprimieren von für reifen BMP-2B kodierender DNA in Säugetierzellen, das die Verwendung der Wirtszelle nach Anspruch 7 umfaßt.

#### Patentansprüche für folgenden Vertragsstaat : ES

- 35 1. Verfahren, umfassend das Konstruieren eines DNA-Hybrid-Konstrukts, das in der 5' nach 3'-Richtung eine DNA-Sequenz für den Vorläuferabschnitt von BMP-2A, die operabel mit einer für reifen BMP-2B kodierenden DNA-Sequenz verbunden ist, aufweist.
- 40 2. Verfahren nach Anspruch 1, worin der Vorläuferabschnitt eine Signalsequenz aufweist.
3. Verfahren nach Anspruch 1 oder 2, worin sowohl BMP-2A als auch BMP-2B menschliche BMPs sind.
4. Verfahren, umfassend das Konstruieren eines Expressionsvektors, umfassend ein DNA-Hybrid-Konstrukt, das in der 5' nach 3'-Richtung eine DNA-Sequenz für den Vorläuferabschnitt von BMP-2A, die  
45 operabel mit einer für reifen BMP-2B kodierenden DNA-Sequenz verbunden ist, aufweist.
5. Verfahren nach Anspruch 4, worin der Vorläuferabschnitt eine Signalsequenz aufweist.
- 50 6. Verfahren nach Anspruch 4 oder 5, worin sowohl BMP-2A als auch BMP-2B menschliche BMPs sind.
7. Verfahren, umfassend die Transformation einer Säugetierwirtszelle mit einem Expressionsvektor, umfassend ein DNA-Hybrid-Konstrukt, das in der 5' nach 3'-Richtung eine DNA-Sequenz für den Vorläuferabschnitt von BMP-2A, die operabel mit einer für reifen BMP-2B kodierenden DNA-Sequenz  
55 verbunden ist, aufweist.
8. Verfahren nach Anspruch 4, worin der Vorläuferabschnitt eine Signalsequenz aufweist.

9. Verfahren nach Anspruch 4 oder 5, worin sowohl BMP-2A als auch BMP-2B menschliche BMPs sind.
10. Verfahren, umfassend das Transformieren einer Säugetierwirtszelle mit dem Expressionsvektor pRK5.bmp2/4-1.1, erhältlich vom Depot ATCC 68.330.
- 5 11. Verfahren, umfassend das Transformieren einer E.coli-Wirtszelle mit dem Expressionsvektor pRK5.bmp2/4-1.1, erhältlich vom Depot ATCC 68.330.
12. Verfahren zum Exprimieren von für reifen BMP-2B kodierender DNA in Säugetierzellen, umfassend die  
10 Verwendung einer Säugetierwirtszelle, die mit einem DNA-Hybrid-Konstrukt, das in der 5' zu 3'-  
Richtung eine DNA-Sequenz für den Vorläuferabschnitt von BMP-2A, die operabel mit einer für reifen  
BMP-2B kodierenden DNA-Sequenz verbunden ist, aufweist, transformiert wurde.
13. Verfahren nach Anspruch 12, worin der Vorläuferabschnitt eine Signalsequenz aufweist.
- 15 14. Verfahren nach Anspruch 12 oder 13, worin sowohl BMP-2A als auch BMP-2B menschliche BMPs sind.
15. Verfahren zum Exprimieren von für reifen BMP-2B kodierender DNA in Säugetierzellen, umfassend die  
20 Verwendung einer Säugetierwirtszelle, die mit dem Expressionsvektor pRK5.bmp2/4-1.1, erhältlich vom  
Depot ATCC 68.330, transformiert wurde.

#### Revendications

Revendications pour les Etats contractants suivants : AT, BE, CH, DE, DK, FR, GB, GR, IT, LI, LU, NL, SE

- 25 1. Produit hybride d'assemblage d'ADN comprenant, dans le sens 5' à 3', une séquence d'ADN pour la  
portion servant de précurseur de la BMP-2A liée de manière fonctionnelle à une séquence d'ADN  
codant pour la BMP-2B mature.
- 30 2. Produit d'assemblage d'ADN suivant la revendication 1, dans lequel la portion servant de précurseur  
comprend une séquence signal.
3. Produit d'assemblage d'ADN suivant la revendication 1 ou la revendication 2, dans lequel la BMP-2A et  
la BMP-2B sont des BMP humaines.
- 35 4. Vecteur d'expression comprenant le produit d'assemblage d'ADN suivant l'une quelconque des  
revendications 1 à 3.
5. Vecteur d'expression qui est le pRK5.bmp 2/4-1.1, disponible sous le numéro de dépôt ATCC 68 330.
- 40 6. Cellule-hôte de mammifère, transformée avec le vecteur d'expression suivant la revendication 4.
7. Cellule-hôte de mammifère, transformée avec le vecteur d'expression suivant la revendication 5.
- 45 8. Cellule-hôte de E. coli transformée avec le vecteur d'expression suivant la revendication 5.
9. Procédé pour l'expression d'un ADN codant pour la BMP-2B mature dans des cellules de mammifère,  
comprenant l'utilisation de la cellule-hôte suivant la revendication 6.
- 50 10. Procédé pour l'expression d'un ADN codant pour la BMP-2B mature dans des cellules de mammifère,  
comprenant l'utilisation de la cellule-hôte suivant la revendication 7.

#### Revendications pour l'Etat contractant suivant : ES

- 55 1. Procédé qui comprend la construction d'un produit hybride d'assemblage d'ADN comprenant, dans le  
sens 5' à 3', une séquence d'ADN pour la portion servant de précurseur de la BMP-2A liée de manière  
fonctionnelle à une séquence d'ADN codant pour la BMP-2B mature.

2. Procédé suivant la revendication 1, dans lequel la portion servant de précurseur comprend une séquence signal.
3. Procédé suivant la revendication 1 ou la revendication 2, dans lequel la BMP-2A et la BMP-2B sont des BMP humaines.
4. Procédé qui comprend la construction d'un vecteur d'expression comprenant un produit hybride d'assemblage d'ADN comprenant, dans le sens 5' à 3', une séquence d'ADN pour la portion servant de précurseur de la BMP-2A liée de manière fonctionnelle à une séquence d'ADN codant pour la BMP-2B mature.
5. Procédé suivant la revendication 4, dans lequel la portion servant de précurseur comprend une séquence signal.
6. Procédé suivant la revendication 4 ou la revendication 5, dans lequel la BMP-2A et la BMP-2B sont des BMP humaines.
7. Procédé comprenant la transformation d'une cellule-hôte de mammifère avec un vecteur d'expression comprenant un produit hybride d'assemblage d'ADN comprenant, dans le sens 5' à 3', une séquence d'ADN pour la portion servant de précurseur de la BMP-2A liée de manière fonctionnelle à une séquence d'ADN codant pour la BMP-2B mature.
8. Procédé suivant la revendication 7, dans lequel la portion servant de précurseur comprend une séquence signal.
9. Procédé suivant la revendication 7 ou la revendication 8, dans lequel la BMP-2A et la BMP-2B sont des BMP humaines.
10. Procédé comprenant la transformation d'une cellule-hôte de mammifère avec le vecteur d'expression pRK5.bmp 2/4-1.1, disponible sous le numéro de dépôt ATCC 68 330.
11. Procédé comprenant la transformation d'une cellule-hôte de E. coli avec le vecteur d'expression pRK5.bmp 2/4-1.1, disponible sous le numéro de dépôt ATCC 68 330.
12. Procédé pour l'expression d'un ADN codant pour la BMP-2B mature dans des cellules de mammifère, comprenant l'utilisation d'une cellule-hôte de mammifère transformée avec un produit hybride d'assemblage d'ADN comprenant, dans le sens 5' à 3', une séquence d'ADN pour la portion servant de précurseur de la BMP-2A liée de manière fonctionnelle à une séquence d'ADN codant pour la BMP-2B mature.
13. Procédé suivant la revendication 12, dans lequel la portion servant de précurseur comprend une séquence signal.
14. Procédé suivant la revendication 12 ou la revendication 13, dans lequel la BMP-2A et la BMP-2B sont des BMP humaines.
15. Procédé pour l'expression d'un ADN codant pour la BMP-2B mature dans des cellules de mammifère, comprenant l'utilisation d'une cellule-hôte de mammifère transformée avec le vecteur d'expression pRK5.bmp 2/4-1.1, disponible sous le numéro de dépôt ATCC 68 330.

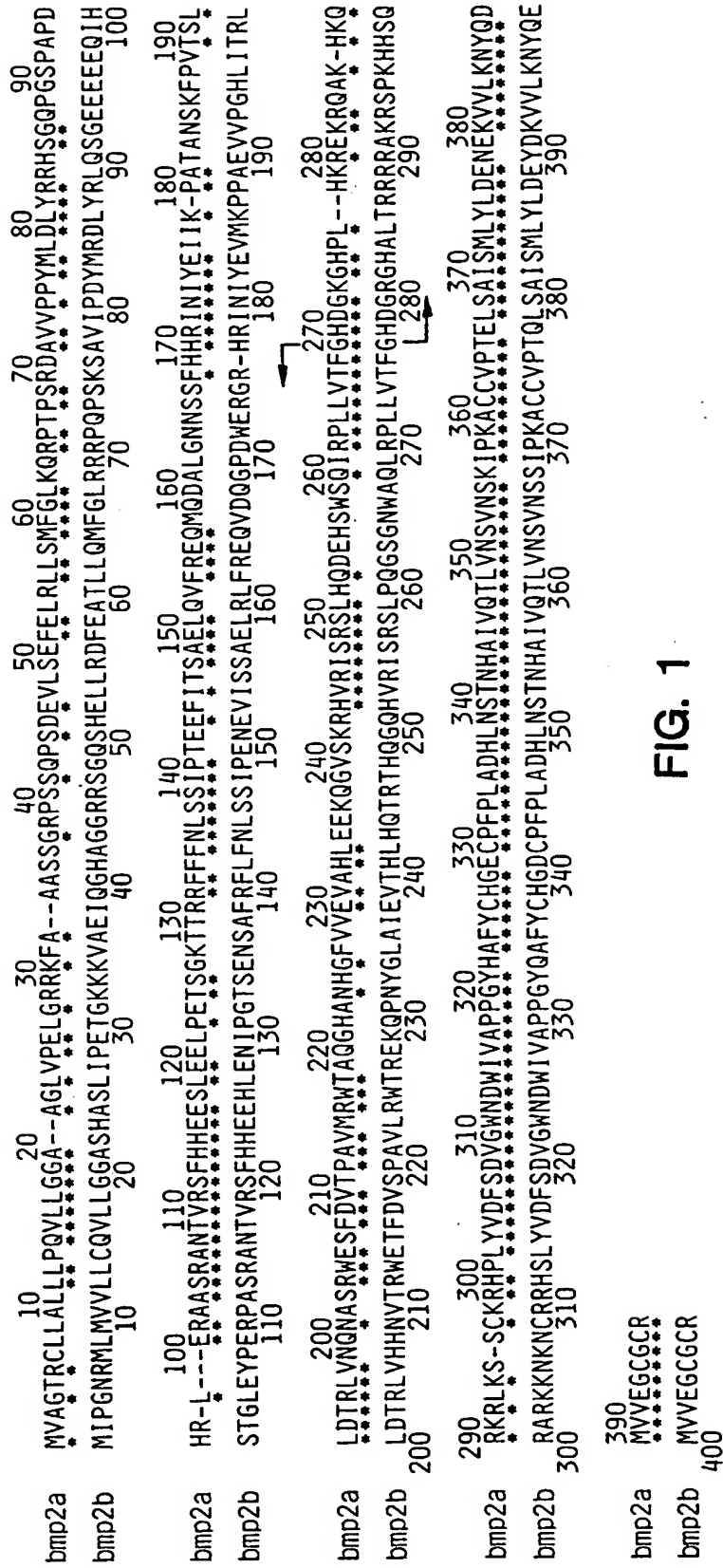


FIG. 1



# FIG. 2

BMP 2A/2B

10	20	30	40	50	60	70
MVAGTRCLLALLPQVLLGGAAGLVPELGRRKFAAASSGRPSSQPSDEVLSEFELRLLSMFGLKQRPTPS						
			RR			
80	90	100	110	120	130	140
RDVVPYMLDLYRRHSGQPGSPAPDHRLEAASRANTVRSFHHEESLEELPETSGKTTRRRFFNLSSIP						
150	160	170	180	190	200	210
TEEFITSAELQVFREOMQDAGNNSSFHHRINIYEIIPATANSKFPVTRLLDTRLVNQNASRWESEFVDVT						
220	230	240	250	260	270	280
PAVMRWTAQGHANHGFEVVAHLEEKQGVSKRHVRISRSIHQDEHSWSQIRPLLVTFGHDGRGHALTRRR						
290	300	310	320	330	340	350
RAKRSPKHHSQRARKKNKNCRRHSLSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNSTNHAIVQ						
360	370	380	390	400		
TLVNSVNSSIPKACCVPTLSAISMLYLDEYDKVVLKNYQEMVVEGCGCR						

FIG. 3A

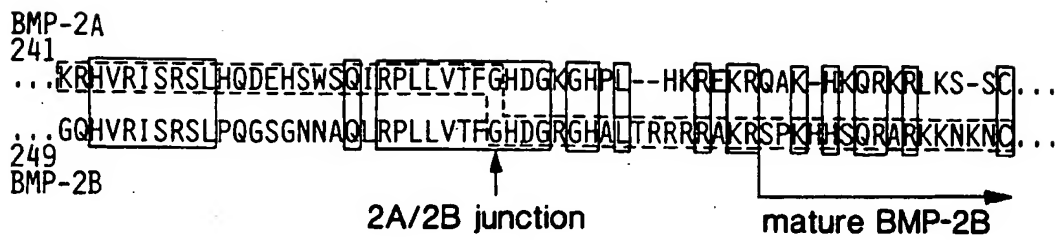
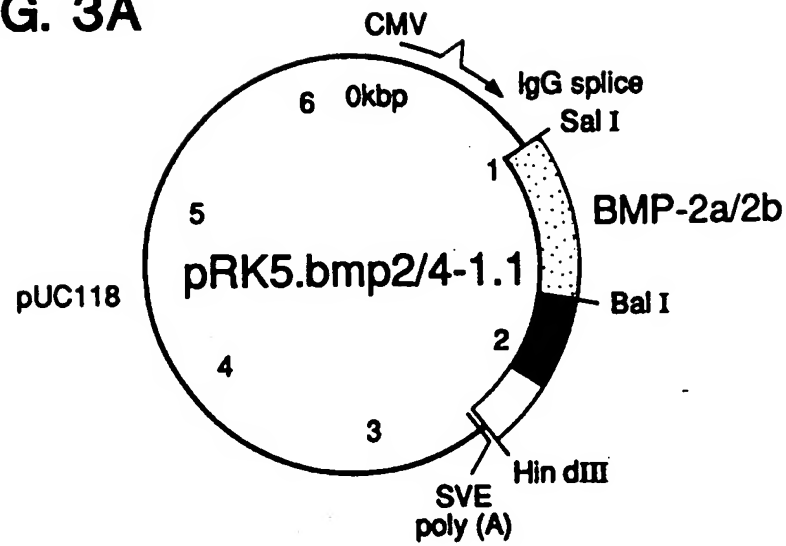


FIG. 3B

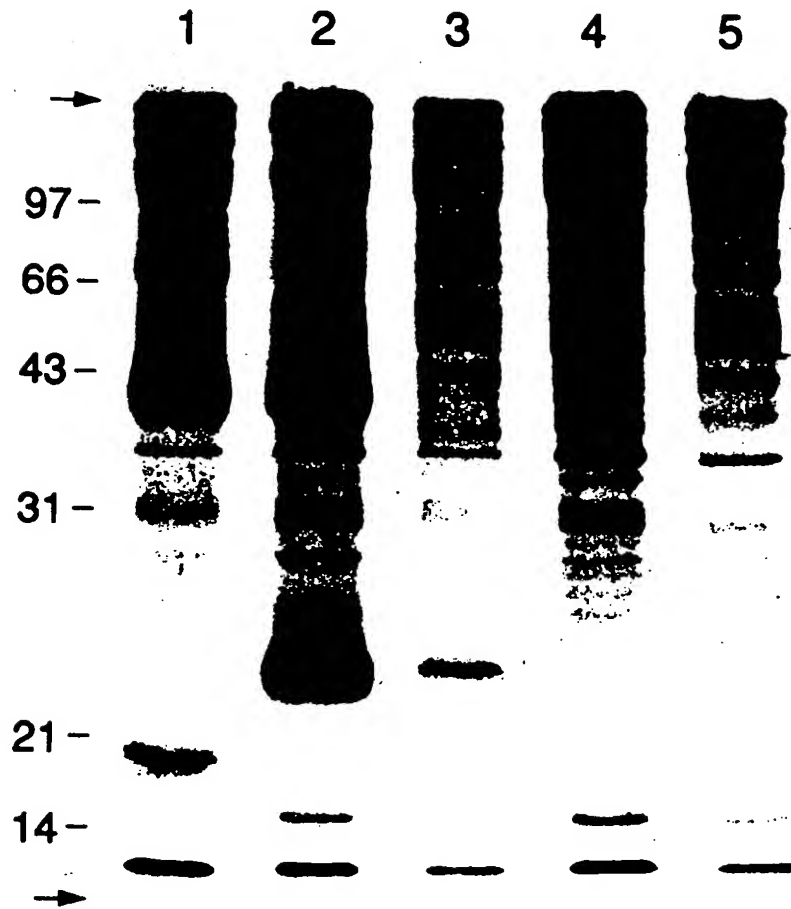


FIG. 4

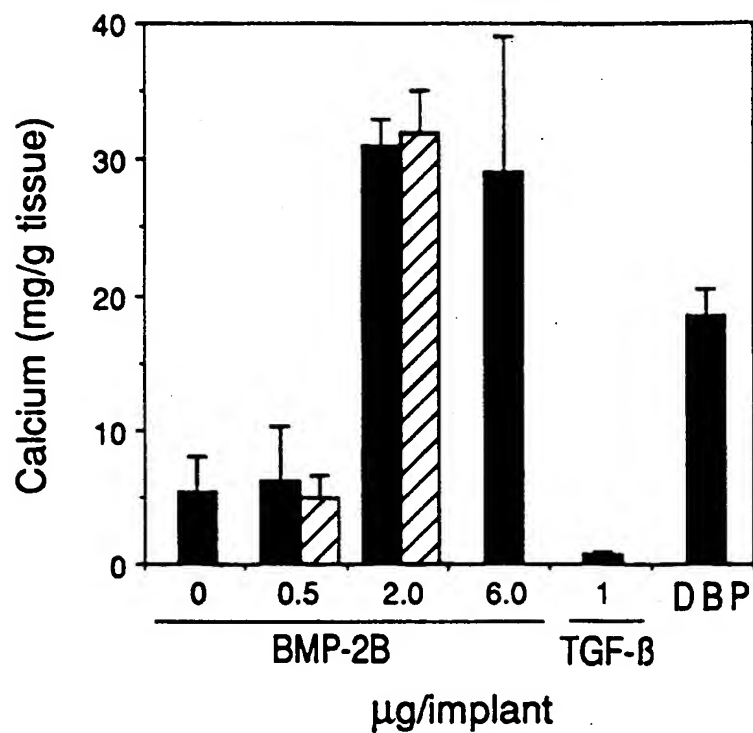


FIG. 5A

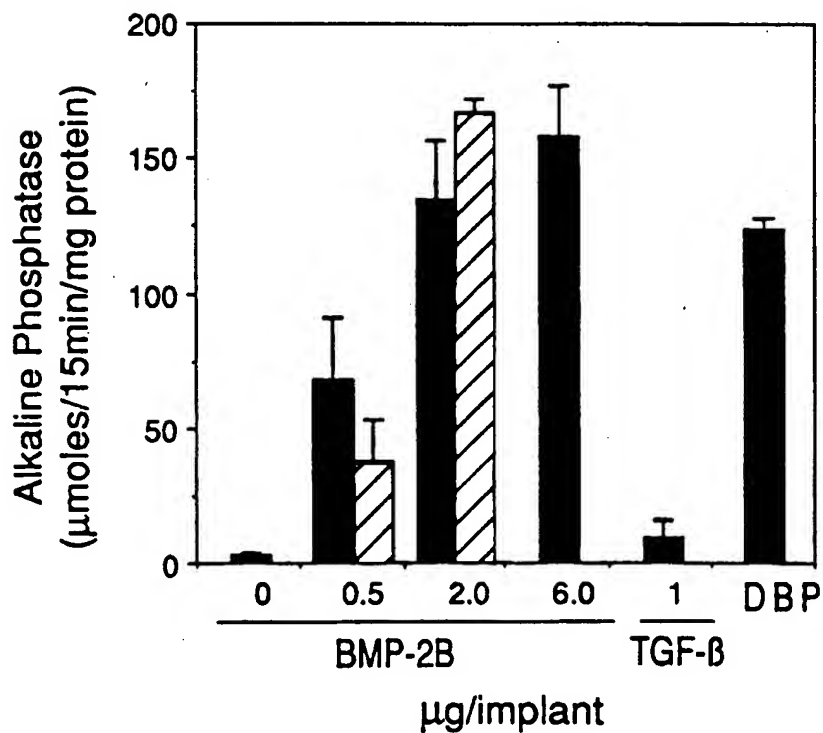


FIG. 5B